

Thu Apr 25 08:07:05 2002

us-09-964-678a-1.rn1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 17:07:56 ; Search time 52.52 Seconds
(Without alignments)
6744.164 Million cell updates/sec

Title: US-09-964-678A-1
Perfect score: 1442
Sequence: 1 ttttttttttgatgagtgag.....ttaacaacagcttagagca 1442

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA.*
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3: /cgn2_6/ptodata/2/lna/6A.COMB.seg.*
4: /cgn2_6/ptodata/2/lna/6B.COMB.seg.*
5: /cgn2_6/ptodata/2/lna/PCITUS.COMB.seg.*
6: /cgn2_6/ptodata/2/lna/Backfiles1.seg.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1442	100.0	1442	US-08-454-557C-120	Sequence 120, App
2	1442	100.0	1442	US-08-340-426D-120	Sequence 120, App
3	1442	100.0	1442	US-08-450-673C-120	Sequence 120, App
4	1233.4	84.8	1418	PCT-US95-17111A-120	Sequence 49, Appl
5	1080.2	74.9	1381	US-08-454-557C-49	Sequence 49, Appl
6	1080.2	74.9	1381	US-08-340-426D-49	Sequence 49, Appl
7	1080.2	74.9	1381	US-08-450-673C-49	Sequence 49, Appl
8	1080.2	74.9	1381	PCT-US95-17111A-9	Sequence 35, Appl
9	475.4	33.0	14796	US-08-975-080-35	Sequence 10, Appl
10	475.4	33.0	14796	US-09-630-706-10	Sequence 3, Appl
11	475.4	33.0	14796	US-09-496-694B-3	Sequence 3, Appl
12	416.4	28.9	55065	US-09-813-817-3	Sequence 101, App
13	400.8	27.8	5543	US-08-687-080-101	Sequence 9, Appl
14	393.6	27.3	4421	US-08-257-963B-9	Sequence 9, Appl
15	393.6	27.3	4421	US-08-367-841A-9	Sequence 9, Appl
16	393.6	27.3	4421	PCT-US95-07201-9	Sequence 1, Appl
17	393.6	27.3	4421	US-08-658-136-2	Sequence 1, Appl
18	393.6	27.3	4421	US-08-658-136-1	Sequence 1, Appl
19	386	26.8	14636	US-08-323-443B-1	Sequence 6, Appl
20	374.6	26.0	14636	US-09-173-914-6	Sequence 28, Appl
21	371.4	25.8	26654	US-09-564-805-28	Sequence 20, Appl
22	367.4	25.5	6769	US-08-480-784-20	Sequence 20, Appl
23	367.4	25.5	6769	US-08-483-553-20	Sequence 20, Appl
24	367.4	25.5	6769	US-08-487-002-20	Sequence 20, Appl
25	367.4	25.5	6769	US-08-483-554B-20	Sequence 20, Appl
26	367.4	25.5	6769	US-08-488-011B-20	Sequence 20, Appl
27	367.4	25.5	6769	US-08-850-727-20	Sequence 20, Appl

28	367.4	25.5	6769	PCT-US95-10202-20	Sequence 20, Appl
29	367.4	25.5	6769	PCT-US95-10220-20	Sequence 20, Appl
30	367.4	25.5	6769	PCT-US95-10220-20	Sequence 6, Appl
31	357.2	24.8	8392	US-08-080-255-6	Sequence 6, Appl
32	357.2	24.8	8392	US-08-465-713-6	Sequence 6, Appl
33	357.2	24.8	8392	PCT-US93-05857-6	Sequence 3, Appl
34	356.8	24.7	8449	US-09-797-906-3	Sequence 63, Appl
35	355.8	24.7	3035	US-08-726-725-2	Sequence 63, Appl
36	354.2	24.6	8342	US-08-545-860D-63	Sequence 7, Appl
37	354.2	24.6	8342	PCT-US94-04496-63	Sequence 7, Appl
38	349.2	24.2	35060	US-08-814-095-7	Sequence 9, Appl
39	349.2	24.0	4421	US-08-257-963B-9	Sequence 9, Appl
40	345.8	24.0	4421	US-08-367-841A-9	Sequence 9, Appl
41	345.8	24.0	4421	PCT-US95-07201-9	Sequence 2, Appl
42	344.2	23.9	3286	US-09-211-417-2	Sequence 1, Appl
43	344	23.9	4803	US-09-197-636-1	Sequence 3, Appl
44	344	23.9	4803	US-09-197-636-3	Sequence 7, Appl
45	342.6	23.8	11811	US-09-078-294-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-454-557C-120
Sequence 120, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
INVENTOR: de la Monte, Suzanne
TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/454,557C
APPLICATION NUMBER: 514
CLASSIFICATION: 514
FILING DATE: 30-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION/DOCKET NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609,3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 1442 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 15..1139
US-08-454-557C-120

Query Match Score 1442; DB 2; Length 1442;
Best Local Similarity 100.0%; Pred No. 0;
Matches 1442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1  RESULT 2
2  US-08-340-426D-120
3  ; Sequence 120, Application US/08340426D
4  ; Patent No. 5948634
5  ; GENERAL INFORMATION:
6  ; APPLICANT: de la Monte, Suzanne
7  ; APPLICANT: Wands, Jack R.
8  ; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
9  ; TITLE OF INVENTION: of Alzheimer's Disease
10 ; NUMBER OF SEQUENCES: 121
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
13 ; STREET: 1100 New York Avenue, Suite 600
14 ; CITY: Washington
15 ; STATE: D.C.
16 ; COUNTRY: U.S.A.
17 ; ZIP: 20005-3934
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: Patent Release #1.0, Version #1.25
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/08/340,426D
25 ; FILING DATE: 14 NOV-1994
26 ; CLASSIFICATION: 435
27 ; ATTORNEY/AGENT INFORMATION:
28 ; NAME: Ludwig, Steven R.
29 ; REGISTRATION NUMBER: 36,203
30 ; REFERENCE/DOCKET NUMBER: 0609.3840002
31 ; TELECOMMUNICATION INFORMATION:
32 ; TELEPHONE: (202) 371-2540
33 ; TELEFAX: (202) 371-2540
34 ; INFORMATION FOR SEQ. ID NO: 120:
35 ; SEQUENCE CHARACTERISTICS:
36 ; LENGTH: 1442 base pairs
37 ; TYPE: nucleic acid
38 ; STRANDEDNESS: double
39 ; TOPOLOGY: both
40 ; MOLECULE TYPE: cDNA
41 ; FEATURE:
42 ; NAME/KEY: CDS
43 ; LOCATION: 15..1139
44 ; US-08-340-426D-120

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RESULT 3
 US-08-450-673C-120
 ; Sequence 120, Application US/08450673C
 ; Patent No. 5948888
 GENERAL INFORMATION:
 APPLICANT: de la Monte, Suzanne
 APPLICANT: Wands, Jack R.
 TITLE OF INVENTION: Neutral thread protein Gene Expression and Detection
 TITLE OF INVENTION: of Alzheimer's Disease
 NUMBER OF SEQUENCES: 121
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,673C
 FILING DATE: 30-MAY-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Ludwig, Steven R.
 REGISTRATION NUMBER: 36,203
 REFERENCE/DOCKET NUMBER: 0609, 3840004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 120:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1442 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: both
 MOLECULE TYPE: cDNA

Query Match	100.0%;	Score 1442;	DB 2;	Length 1442;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1442:	Conserved 1442;			

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Db      1441  ca 1442

RESULT      4
PCT-US95-17111A-120
; Sequence 120 Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-3200

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[illegible]

RESULT 5
US-08-454-557C-49
Sequence 49, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609,3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

us-09-964-678a-1

Query Match	74.9%;	Score 1080.2;	DB 2;	Length 1381;
Best Local Similarity	94.4%;			
Matches 1317;	Conservation	Pred. No. 4.8e-292;		

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Page 6

RESULT 6
 US-08-340-426D-49
 Sequence 49, Application US/08340426D
 Patent No. 5948634
 GENERAL INFORMATION:
 APPLICANT: de la Monte, Suzanne
 APPLICANT: Wands, Jack R.
 TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
 NUMBER OF SEQUENCES: 121
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/340,426D
 FILING DATE: 14-NOV-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ludwig, Steven R.
 REGISTRATION NUMBER: 36, 203
 REFERENCE/DOCKET NUMBER: 0609, 3840002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 49:
 LENGTH: 1381 bases

us-09-964-678a-1.rni

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Oy	1012	; Sequence 35, Application US/08975080	
Dc	1013	Patent No. 6245523	
Oy	1072	GENERAL INFORMATION:	
Dc	1071	APPLICANT: Altierl, Dario C.	
Oy	1131	TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS	
Dc	1129	TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION	
Oy	1191	NUMBER OF SEQUENCES: 35	
Dc	1189	CORRESPONDENCE ADDRESS:	
Oy	1311	ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP	
Dc	1307	STREET: 1800 M Street, N.W.	
Oy	1371	CITY: Washington	
Dc	1367	STATE: D.C.	
Oy	1367	COUNTRY: USA	
Dc	1367	ZIP: 20036-5869	
Oy	1367	COMPUTER READABLE FORM:	
Dc	1367	MEDIUM TYPE: Floppy disk	
Oy	1367	COMPUTER: IBM PC compatible	
Dc	1367	OPERATING SYSTEM: PC-DOS/MS-DOS	
Oy	1367	SOFTWARE: Patentn Release #1.0, Version #1.30	
Dc	1367	CURRENT APPLICATION DATA:	
Oy	1367	APPLICATION NUMBER: US/08/975,080	
Dc	1367	FILING DATE: 20-NOV-1997	
Oy	1367	PRIOR APPLICATION DATA:	
Dc	1367	APPLICATION NUMBER: US 60/031,435	
Oy	1367	FILING DATE: 20-NOV-1996	
Dc	1367	ATTORNEY/AGENT INFORMATION:	
Oy	1367	NAME: Adler, Reid G.	
Dc	1367	REGISTRATION NUMBER: 30,988	
Oy	1367	REFERENCE/DOCKET NUMBER: 044574-5022-01-WO	
Dc	1367	TELECOMMUNICATION INFORMATION:	
Oy	1367	TELEPHONE: 202-467-7176	
Dc	1367	TELEFAX: 202-467-7176	
Oy	1367	INFORMATION FOR SEQ ID NO: 35:	
Dc	1367	SEQUENCE CHARACTERISTICS:	
Oy	1367	LENGTH: 14796 base pairs	
Dc	1367	TYPE: nucleic acid	
Oy	1367	STRANDEDNESS: single	
Dc	1367	TOPOLOGY: linear	
Oy	1367	MOLECULE TYPE: DNA (genomic)	
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ULT 9
 08-975-080-35
 Sequence 35, Application US/08975080
 Patent No. 6245523
 GENERAL INFORMATION:
 APPLICANT: Attiari, Dario C.
 TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
 CELLULAR APOPTOSIS, AND ITS MODULATION
 TITLE OF SEQUENCES: 35
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
 STREET: 1800 M Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20036-5869
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/975,080
 FILING DATE: 20-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/031,435
 FILING DATE: 20-NOV-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Adler, Reid G.
 REGISTRATION NUMBER: 30,988
 REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-467-7000
 TELEFAX: 202-467-7176
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14796 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 1S-08-975-080-35

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RESULT 10
US-09-630-706-10
; Sequence 10, Application US/09630706
; Patent No. 6277640
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: lex M. Cowserl
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION
; FILE REFERENCE: RTS-0053
; CURRENT APPLICATION NUMBER: US/09/630.706
; CURRENT FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 10
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
US-09-630-706-10

Query Match
Best Local Similarity 33.0%; Score 475.4; DB 4; Length 14796;
Matches 877; Conservative 0; Mismatches 321; Indels 59; Gaps 15;

OY 1 ttttttttttgaatggaatgttctgcctctgtgtgccaggcgtcgagatgcaatggtgcga 60
Db 5380 ttttttttttgcagatagag-tttcaactctgtgtcccaaggctgagtgcaatgtgcaa 60
OY 61 tctaacgtcacgcgaacctgcgcctccgggttcaaagcatctcctcgtcgaagctccc 120
Db 5439 tcttggtcactcagcaacctcgtcctcgtgggtcgaagtatctctcgtcccaagctccc 120
OY 121 cagtagctggagatcaaggcatgtgcaaccaagctcgcgataatttggatatttttttag 180
Db 5499 aagtaactggtgagatcaagggaagtgcacacaaacccagctaatltt--tggatttttag 180
OY 181 tagagatggagatttcacatgtttgttcaggtgtgtctcgaactcccgactcagatgagtc 240
Db 5556 tagagatggagatttcacacacattgccagagctgtgtcttgaacttcctgaactc--gtgalt 5613
OY 241 cctcgcctcggcctcccaaaagtgtagatagacagagatggccacatgcccggtctgc 300
Db 5614 cgcacacctgtgcccctccaaagtgtcg--gattcaaggcgtgaaccacacacagcgtgagc 5670
OY 301 tggatcaattttgtgtagaaacagggttcaactgaatgtgccaagctgtctcctg--- 357
Db 5671 ttttttttttgttct-gagacacagtttcaactcgttaccacagcgtggagtagggtag 5729

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Query Match	33.0%	Score 475.4	DB 4	Length 14796
Best Local Similarity	69.8%	Pred. No. 7.9e-123	Indels 59	Gaps 15
Matches 877	Conservative 0	Mismatches 321		
<p>SEQ ID NO 3 LENGTH: 14796 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (2811)...(2921) NAME/KEY: CDS LOCATION: (3174)...(3283) NAME/KEY: CDS LOCATION: (5158)...(5275) NAME/KEY: CDS LOCATION: (11955)...(12044) US-09-496-694B-3</p>				
Query	1	ttttttttttagatgagatttcgtctcttttggccacgcggagatgcaatgacgca	60	
DB	5380	ttttttttttagatagag-tttcaactctgtttgcacagcgagatgcaatgacgca	5438	
QY	61	tctcagctcacgcaaacctccgcctcccggttcaagagattctctgctcaagccccc	120	
DB	5439	tcttgcccaactgcaaacctctgcctccgcgttcaagtattctctgctccagccccc	5498	
QY	121	caatgacgtggaattacagagcatgtgacaccacgcctcggaataatttgaattttt	180	
DB	5499	aagtaactggaattacaggaagatgcccacacacagctaatttt-tgatttttag	5555	
QY	181	tagagatggaattttccatgtgtgtcagcgtgtctcgaaactccgcagccctcagaatg	240	
DB	5556	tagaagctggggttttccaccacatgtgccagagctgtcttgaactcttgacctc--gtgatt	5613	
QY	241	cctccgtctcgcgcctcccaaatgctagatataaggaactgcccacatgcccgcgtctgc	300	
DB	5614	cgcgcacacttgcctcccaaatgctcgcg--gattcaaggctgtaaccacacagcgtgc	5670	
QY	301	tgagctaattttggtagaacaagggttccactgtatgcccagctgtctcgt---	357	
DB	5671	tttttttttctgtct-gagacaacagttactctgttaaccagagctgagtaggtg	5729	
QY	358	--agctcaagcagttccacctcgtgcctcagccctcccaaatgctgtagatatacagcgctgacg	415	
DB	5730	cctgactcgtacatcagtcacacactccgcctccgcgtggtcgaagtgaatttgcgtcttcagc	5789	
QY	416	ctgtcgcgtgcctttttattttttttttaagaacaagtgltccaccttaccacga	475	
DB	5790	ctcccaagtagcgaagattacagcagtggtccaccacacacagtgaaattttgtaattt	5849	
QY	476	tgaagtgcagtggtgtgata--cagctcactgcagccttcaactcttgatatac--ca	532	
DB	5850	gttagagcagaggtttccacatgttggccaaagctgtgttttgaactctcgtacactgaagtga	5909	
QY	533	tctctcgtcctcagcctcccaagtagcgtgggacccaagaatgacacatgacacactctgac	591	
DB	5910	tccaccgcgctcagcctcccaaatgctcgtgagatatagtgtgagccacacacacttggcc	5969	
QY	592	-----caattttattttatttttaatttttttttttttttttttttttttttttttt	640	
DB	5970	tcaggaagatt	6028	
QY	641	caccacagctgtagagtgagtgacgaacatttgctcaactgcaacctctgctcccggtt	700	
DB	6029	cgcgcagcttagagtgacgaacaggtactcgtcctacatcagtcgaagctccgcgcccaaggtt	6088	

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RESULT 12
US-09-813-817-3/C
; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: IAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO01178
; CURRENT APPLICATION NUMBER: US/09/813,817
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

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Db 15043 ATTTT---TGTAATTTTGTAGAGACAAGTTTCACCATGTTGGCCAGGCTGGTCTGGAA 14987

QY 222 CTCGCCACCTCAGATGATCCTCTCGCTCGCTCGCTCCCAAGTgct-agaTaaaggaTg 280

Db 14986 CTCTCTACCTCAGTGTATCCGCCGCTCTGACCTCCCAAGTCTGGGATTTACAGGCGCG 14927

QY 281 CCGCAATGCGCGCTCGCTCGCTgctaatttttgTgTgaagaacaggttttaactgTg 340

Db 14926 AAGCACCGCGCCCAACCTCCATTTTTTTTTTTTTTTGTAGACAAAGTCTTGCTGTGCG 14867

QY 341 CCGCAAGTg-----gTctctgagTca 363

Db 14866 CCCAGCGTGCATGCGATGGCGCATCTCAGCTCAGTCCAAAGTCTCCGCTCCCGGTTTCA 14807

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QY 422 TgCGCTTTaattttattttttttaaGacaagTgTcccaactttaaccaagTgaagT 481

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QY 771 tTtgatattttagTaaagaTgggT-tTcaacatgTgcgaagTgTgcttgatcctg 829

Db 14390 TTTGATTTTGAATTGATGATGGGCTTACACATGTTGGCAGAGCTTAATCTCGAATCTCTG 14331

QY 830 acct- TgTgaTcTgCctgCctgCctcccaagTgctggaTtaacagcgTgaagcCac 887

Db 14330 ACCTCAAGTATCCACTGCTTGCTCCCAAAAGTCTGGGATTTACTGGCGTAGACAA 14271

QY 888 CAGGCGCGgcttaatt-tTaatttgTgtTgTgaatTgaatTcaactcactgTttacca 946

Db 14270 CGGCGCTGGCTCTTCTTTTTTTTTTTTTTTTTTTGTAGATAAAGGCTTGGCTCTGTCTATCA 14211

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Db 14210 GCGCTGCACTAGTATGCTGATGAGTATGCTTACAGCGCTCAACCTCTCGGCTCAAGA 14151

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Db 14030 CTCCTGAATTAAGCAATCTCCCGCTAGGCTCCCAAAAGTGTGATATTATTAAGTGA 13971

QY 1186 agcc 1189

Db 13970 AGCC 13967

[illegible]

RESULT 14
 US-08-257-963B-9
 Sequence 9, Application US/08257963B
 Patent No. 5840686
 GENERAL INFORMATION:
 APPLICANT: Chader, Gerald J.; Becerra, S.,
 Patricia, Schwartz, Joan P.;
 APPLICANT: Taniwaki, Takayuki
 TITLE OF INVENTION: PIGMENT EPITHELIN
 TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
 TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
 TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan & Flinnegan
 STREET: 345 Park Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/257,963B
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:

Query Match	27.3%	Score 393.6	DB 2	Length 4421
Best Local Similarity	82.8%	Pred. No. 3.1e-100		
Matches 512	Conservative 0	Mismatches 94	Indels 12	Gaps 5
QY 556	tttatatttatttatttatttattttagagacagagctaaactcgttaacccaggctgagat	655		
Db 3485	TCCTAGATTTTCTTTTCTTTCTTTGAAATGAGCTCTGGCTGTGATCCACCAAGCTTGAGT	3543		
QY 656	gcagtagggagaaatttggctcctcaatctgcaacctcgtccctcgggtttcaagtattcccg	715		
Db 3544	GCAATGGCGGCAATCGGGCTACCTAGCAAGCTCTTCCTCCGGGGTCAACCCATTCTCCG	3603		
QY 716	ccccagcctcctgaatagctcgtgagactacagggc---ccacacagcgtctaattttt	772		
Db 3604	CCCTCAACCTCCGAGTAGCTGTGAATACAGGCGCTCCGCCACACAGCGCCGACTAAATTTT	3663		
QY 773	tgatttttagtagagatagggttcaacatgctcgcaggttgaactgtatcctgtgac	831		
Db 3664	TGTATTTTAGTAGAARCGGGGTTTACCGTGTTAGCCAGATGGCTGTGATCTGTGAC	3723		
QY 832	ctgtgatctgcctgcctcgcgcctcccaagcgtcgggattacaaggcgttgagccacag	891		
Db 3724	CTCTGATATGTGCTCGCTCGGCTCCCAAGTGTGGGATTAACAGGCTTGAGCCACCGCA	3783		
QY 892	cccgagctattttaaattttgttgtttgaatggaactcactcgttgttaaccaggct	951		
Db 3784	CCGGGCTCTTATTTTTTTT-----TTTGGATGGAGTCTCAACATGTACCTGGGCTG	3837		
QY 952	gagtgcaatgagccaaatcctcgtcctcaatctgcaacctcgtcccggtctaaagatct	1011		
Db 3838	GAGTCCAGTGGAGCATCTCGGCTACCTGCAACCTCCGCCCTCGGGGTAAAGATTTCT	3897		
QY 1012	cctgtcctcagcctcccaagcgtcgggattacaggcaccctgcaaccaaccccgtcta-at	1070		
Db 3898	CTGTGCTACGCTCCCAAGTAGTGTGGGATTAACAGGTGCCACCAACACGCGCTGGTAAGT	3957		
QY 1071	tttgttatattcatttagaggcgggtttcaacatatattgccaagctggtctcaactcct	1130		
Db 3958	TTTTGTATTTTAAAGATGGGTTTCAACATGTTGGCCAGCGCTGTGAATCTCT	4017		
QY 1131	gacctcaggtagaacccacctgctcccaagccttccaaagtctgggattacagcgttagaca	1190		
Db 4018	GACATCAGTGTGATCCGGCCACTTACCTCCCAAAGTCTGGGATTAACAGGGGTAGCCA	4077		
QY 1191	cctcaaccagcccggtctaa 1208			

	Query Match	27.3%	Score 393.6	DB 4	Length 4421
Best Local Similarity	82.8%	Pred. No. 3,1e-100			
Matches 512	Conservative 0	Mismatches 94	Indels 12	Gaps 5	
QY	596	tttatatttatatttaatttttagcagacagctcaactcgtccaccagcttgatg	655		
Db	3485	TCTTAGATTTTTTTTTTCTTTAGATGAGACT-GGCTGTGTACACGACGCTGAT	3543		
OY	656	gcagctggcgcaactcttggtcactcagccctcgtccccgggttaagttattctcctg	715		

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Db 3544 GCAGTGGCGCGATCTCGGCTCACTGCAACCTCTTCTCCCGGGTTACCCCATTCCTCTG 3603
QY 716 cccagcctcctagtagctggactacagcg---ccacacgcctagctaatltt 772
Db 3604 CCTCAACCTCCCGAGTAGTGTGAATACAGGGCTCCGCCACACGCGCACTAATTTT 3663
QY 773 tgaattttagtagagatggg-ttaaccaagtctgccaagttgactctgac 831
Db 3664 TGTATTTTATAGAGACGCGGGTTTCACCGTGTACCGAGATGCTGTGATCTCTGAC 3723
QY 832 ctgtgaatctgctgctcgccctcccaagtgctggatlaacaagcgtgagccacag 891
Db 3724 CTGCGATCTGCTGCTGCTGCGCTCCCAAGTCTGTGATACAGGCTTGAGCCACGCA 3783
QY 892 cccgactaatttlaatttltgttgtgaatgaaatcactctgttaaccagctg 951
Db 3784 CCGGCTCTTATTTT-----TTGAGATGAGTCTCACACTGTACCTGCGGCTG 3837
QY 952 gagtgaatggccaatctcgctcactgaacctctgctcccggtcgaagcattct 1011
Db 3838 GAGTGCAGTGGAGCGATCTCGGCTCACTGCAACCTCGGCTCTCGGGTTCAAGAGATCT 3897
QY 1012 cctgtctcagcctcccaacagctgggattacgggacctgccaaccaaccgccta-at 1070
Db 3898 CTGCTCTCAGCTCCCAAGTAGCTGGGATTACAGTGCACACACAGCGCTGTAGTT 3957
QY 1071 ttgttatttcaatagagcggggttcaacaatttgcaggctgctcaactcct 1130
Db 3958 TTTTGTATTTTATGTAAGATGGGTTTCACCATGTTGGCAGGCTGTGACTCTCT 4017
QY 1131 gacctcaagtgaccacacgctcctcaagcttccaaagtgtggaattacaagcgtgagcca 1190
Db 4018 GACATCAGGTGATCCGCCACCTTAGCCTCCCAAGTGTGGAATTACAGGCGTGAAGCA 4077
QY 1191 cctcaccagccggtcta 1208
Db 4078 CCATACCTGGCCAGCAA 4095
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Search completed: April 24, 2002, 19:37:30
Job time: 8974 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 17:05:21 ; Search time 1728.26 Seconds
(without alignments)
17460.374 Million cell updates/sec

Title: us-09-964-678a-1
Perfect score: 1442
Sequence: 1 ttttttttttgatgatgag.....ttaacaagcttagagca 1442

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.Da.*
2: gb.Htg.*
3: gb.In.*
4: gb.Om.*
5: gb.Ov.*
6: gb.Pat.*
7: gb.Ph.*
8: gb.Pl.*
9: gb.Pr.*
10: gb.Ro.*
11: gb.Sts.*
12: gb.Sy.*
13: gb.Un.*
14: gb.Vi.*
15: em.Da.*
16: em.Fun.*
17: em.Hum.*
18: em.In.*
19: em.Mu.*
20: em.Om.*
21: em.Or.*
22: em.Ov.*
23: em.Pat.*
24: em.Ph.*
25: em.Pl.*
26: em.Ro.*
27: em.Sts.*
28: em.Un.*
29: em.Vi.*
30: em.Htg.Hum.*
31: em.Htg.Inv.*
32: em.Htg.Other.*
33: em.Htgo.Inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Score Length DB ID Description

1	1442	100.0	1442	6	AR051550	Sequence
2	1442	100.0	1442	6	AR072690	Sequence
3	1442	100.0	1442	6	AR073235	Sequence
4	1442	100.0	1442	6	AF010144	Homo sapi
5	1301.4	90.2	124001	9	HS886K2	Human DNA
6	1080.2	74.9	1381	6	AR051479	Sequence
7	1080.2	74.9	1381	6	AR072619	Sequence
8	1080.2	74.9	1381	6	AR073164	Sequence
9	592.2	41.1	160714	2	AC087434	Pan trogl
10	590.4	40.9	99370	2	AC005057	Homo sapi
11	587.8	40.8	65608	6	AX330738	Sequence
12	587.8	40.8	65608	6	AX332242	Sequence
13	587.8	40.8	65608	6	AX335496	Sequence
14	587.8	40.8	65608	6	HS062293	Human LIM-K
15	587.8	40.8	67046	9	HS063721	Human elast
16	587.8	40.8	148525	2	AC016675	Homo sapi
17	578.4	40.1	121272	2	AC004865	Homo sapi
18	567.6	39.4	170630	2	AC016905	Homo sapi
19	567.6	39.4	201300	9	AL137073	Human DNA
20	562.4	39.0	212956	2	AC090543	Homo sapi
21	558.2	38.7	129169	2	AC032038	Homo sapi
22	556.8	38.6	148478	2	AC026687	Homo sapi
23	556.8	38.6	137737	9	AC010378	Homo sapi
24	556.4	38.6	192330	2	AL590133	Homo sapi
25	555	38.5	91927	9	AC004771	Homo sapi
26	554.6	38.5	42665	9	AC011559	Homo sapi
27	551.8	38.3	211063	2	AC069254	Homo sapi
28	550.8	38.2	155949	9	AC091022	Homo sapi
29	550.8	38.2	156863	9	AC069249	Homo sapi
30	550.4	38.2	94121	9	HS1153P9	Human DNA
31	550.2	38.2	193897	2	AC068486	Homo sapi
32	548.2	38.0	174864	2	AC026125	Homo sapi
33	548.2	38.0	206052	2	AC010173	Homo sapi
34	545	37.8	173240	2	AC021586	Homo sapi
35	543.8	37.7	123146	9	AC011736	Homo sapi
36	541.2	37.5	62485	9	AL590093	Human DNA
37	540.2	37.5	171056	2	AC026318	Homo sapi
38	540.2	37.5	172248	2	AC012466	Homo sapi
39	538.2	37.3	129043	9	CNS01DITD	Human chr
40	538.2	37.3	191946	9	CNS01DITK	Human chr
41	537.2	37.3	110129	9	AC008956	Homo sapi
42	535.2	37.1	79528	9	HS466N1	Human DNA s
43	535.2	37.1	134896	9	AC006571	Homo sapi
44	535.2	37.1	150296	9	HT091326	Human Chrom
45	534.8	37.1	112337	2	AC011509	Homo sapi

ALIGNMENTS

RESULT	1
LOCUS	AR051550
DEFINITION	Sequence 120 from patent US 5830670.
ACCESSION	AR051550
VERSION	AR051550.1 GI:5974914
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 1442)
AUTHORS	de la Monte,S. and Wands,J.R.
TITLE	Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL	Patent: US 5830670-A 120 03-NOV-1998;
FEATURES	Location/Qualifiers
source	1..1442
BASE COUNT	314 a 402 c 311 g 415 t
ORIGIN	/organism="unknown"

Query Match 100.0% Score 1442; DB 6; Length 1442;

Db	1321	CAATTTTAAACGTTACACTTATTTAGTATCTGAATAAGTAAATACATTAACATGT	1380
QY	1381	caaacctgcgaattccgtagttaaagagatctttaaactttaacaagctttag	1440
Db	1381	CAAACTCGCAAAATTCAGTAACTAAACAGAGTCTTTTAACTTTTAAACAACTTTAG	1440
QY	1441	ca 1442	
Db	1441	CA 1442	
RESULT	3		
LOCUS	AR073235	1442 bp	DNA
DEFINITION	Sequence 120 from patent US 594888.		linear
ACCESSION	AR073235		
VERSION	AR073235.1	GI:999998	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1442)		
AUTHORS	la Monte,S. and Wands,J.R.		
TITLE	Neural thread protein gene expression and detection of Alzheimer's disease		
JOURNAL	Patent: US 594888-A 120 07-SEP-1999;		
FEATURES	Location/Qualifiers		
source	1..1442		
BASE COUNT	314 a 402 c 311 g 415 t		
ORIGIN			
Query Match	100.0%;	Score 1442;	DB 6; Length 1442;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 1442;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	tttttttttttgagatggaatttttgctctgtgtgcccagagctgagatggaatggcgaa	60
Db	1	TTTTTTTTTTGAGATGAGAGTTTGCTTGTCTGTCCAGGCTGAGTGCATGCGCAA	60
QY	61	tctcaactcaaccgcaacctccgctccggatgtaacgatatcttcctccagctccc	120
Db	61	TCGACGTCCGCCAACGCTCCGCTCCGGTTCAAGGAGTTCTCTCTCCACGCTGCC	120
QY	121	cagtagctggaattacaagcattgtgaccacgctcggctaaatttgtatttttttag	180
Db	121	CAGTAGCTGGGATTTACAGGCATGTGCACCCACGCTTGCTAATTTGTATTTTATAG	180
QY	181	taagataggagattctcatalgttgtaagcgtgtgtctgaactccgacctaaagtac	240
Db	181	TAGAGATGAGATTCTTCCATGTTGGTCAAGCTGCTCGAATCCGACCTCAGATGATC	240
QY	241	cctccgtctcgagctcccaagatgctatgatacaggaatgccaacatgcccagcttgc	300
Db	241	CCTCGCTCGGCCCTCCAAAGTCTAGATACAGAGACTGGCCACATGGCCGCTGTGCC	300
QY	301	tggctaatattgtgtgtagaacaagggtttcaactgattgcccagaagtgtctccagag	360
Db	301	TGGCTAATTTTGTGTGAGAAACAGGGTTTCACTGATGTGCCAAGCTGGTCTCTGAGC	360
QY	361	tcaagcagtcacactgcgctcagcctccccaagaatgcttggaattacaaggcgtgcag	420
Db	361	TCAAGCAGTCCACCTGCTCAGCTCCCAAGTGTGGATTTAGACAGGCGTGCACCGCTGC	420
QY	421	ctggcctttatattattttttttaagaacagatgtccacacttaccagaatgaa	480
Db	421	CTGGCCTTTTATTTATTTTATTTTAAACACAGGGTGCTCCACTTTACCAAGATGAAG	480
QY	481	tgcagtgatgtatcaacagctactcaactcaactcctcagatcaagcactctctg	540
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[illegible]

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[illegible]

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DB 1247 TGCCCAAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCT 1246
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RESULT 7
LOCUS AR072619 1381 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 49 from patent US 5948634.
ACCESSION AR072619
VERSION AR072619.1 GI:9999383
KEYWORDS

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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1381)
AUTHORS de la Monte,S., and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's
JOURNAL Patent: US 5948634-A 49 07-SEP-1999;
FEATURES
source Location/Qualifiers
BASE COUNT 296 a 384 c 302 g 399 t
ORIGIN

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Query Match
Best Local Similarity 74.9%; Score 1080.2; DB 6; Length 1381;
Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;

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Db 1367 ATAACATGTCAAAC 1381

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RESULT 9
LOCUS AC087434 160714 bp DNA linear HTG 05-JAN-2001
DEFINITION Pan troglodytes clone RP43-90F9, WORKING DRAFT SEQUENCE, 12
ACCESSION AC087434.1 GI:12039251
VERSION AC087434.1
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE chimpanzee.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
1 (bases 1 to 160714)
REFERENCE
AUTHORS Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.,
Gautfarth,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Grante,S.,
Guan,X., Gupta,J., Ho,S.-L., Idol,J.R., Karlins,E., Lee-Lin,S.-Q.,
Legaspi,R., Llm,M., Maduro,Q.L., Maduro,V.B., Mastello,C.,
Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,W., Prasad,A.,
Shenchenko,Y., Snyder,B., Stancilpop,S., Thomas,J.W., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Wetherly,K.D., Zhang,L.-H. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 160714)
Green,E.D.
DIRECT SUBMISSION
Submitted (05-JAN-2001) NIH Intramural Sequencing Center, 8717
Groveomont Circle, Gaithersburg, MD 20877, USA
COMMENT
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.mouse@nigrl.nih.gov
----- Project Information
Center project name: aod
Center clone name: 090F09
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 15263 bases at least Q40
Consensus quality: 15437 bases at least Q30
Consensus quality: 15572 bases at least Q20
Insert size: 13700; agarose-fp
Insert size: 13700; pulse-field-gel
Insert size: 159614; sum-of-ctrls
Quality coverage: 9.32x in Q20 bases; agarose-fp
Quality coverage: 9.32x in Q20 bases; pulse-field-gel
Quality coverage: 8.00x in Q20 bases; sum-of-ctrls

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* NOTE: This is a 'working draft' sequence. It currently
 * consists of 12 contigs. The true order of the pieces
 * is not known and their order in this sequence record is

```

* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 2808: contig of 2808 bp in length
* 2809: gap of unknown length
* 6190: contig of 3282 bp in length
* 6191: gap of unknown length
* 6291: contig of 6248 bp in length
* 12539: gap of unknown length
* 12638: gap of unknown length
* 12639: contig of 8177 bp in length
* 20816: gap of unknown length
* 20916: contig of 8066 bp in length
* 28982: gap of unknown length
* 29082: gap of unknown length
* 40699: contig of 11618 bp in length
* 40700: gap of unknown length
* 40800: contig of 8721 bp in length
* 49520: gap of unknown length
* 49521: contig of 12927 bp in length
* 49621: gap of unknown length
* 62548: contig of 13818 bp in length
* 62648: gap of unknown length
* 76466: contig of 21712 bp in length
* 76566: gap of unknown length
* 98378: gap of unknown length
* 98378: contig of 28797 bp in length
* 127175: 160714: gap of unknown length
* 127275: 160714: contig of 33440 bp in length.
Location/Qualifiers
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Best Local Similarity 71.2%; Pred. No. 1.6e-165;
Matches 944; Conservative 0; Mismatches 348; Indels 33; Gaps 11;
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Db 132561 TTTTGTGAGATGAGAGATT-T-GCCTTGTTGCCAGGCTCAAGTGTATGCGACAGACT 132619
Qy 64 cagtcacgcgaactccgcctccgggttcaagcagattctctgctcagcctcccaag 123

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restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/CTB/CHR7/>, send <mailto:sgreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
Clone CTB-52H6 is from the first release of the human BAC library CTB-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc. (<http://www.resgen.com>).
VECTOR: pBelobAC11
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is CTA-270D13. Actual start of this clone is at base position 135330 of CTA-270D13; actual end is at base position 99370 of CTB-52H6.

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 REFERENCE
 1 (sites)
 Young, P.E., Augustus, M., Carter, K.C., Eber, R., Endress, G.,
 Horrikan, S., Soppet, D.R. and Weaver, Z.
 Cancer gene determination and therapeutic screening using signature
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 JOURNAL
 Avalon Pharmaceuticals (US)
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Search completed: April 24, 2002, 19:40:35
 Job time: 9314 sec

Thu Apr 25 08:07:04 2002

us-09-964-678a-1.rge

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK nucleic - nucleic search, using sw model

Run on: April 24, 2002, 17:03:15 ; Search time 1503.67 Seconds
(without alignments)
12943.405 Million cell updates/sec

Title: US-09-964-678a-1

Perfect score: 1442
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum:*
3: em_estin:*
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7: em_estro:*
8: em_hic:*
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11: gb_hic:*
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16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	378.4	26.2	767	9	AV700498	AV700498 AV700498
5	373.8	25.9	658	12	A0393450	A0393450 CITR1-El-
6	373	25.6	911	12	A0746594	A0746594 HS.2278.A
7	368.8	25.6	970	10	BM468547	BM468547 AGENCOURT
8	367.6	25.5	5556	12	A0839814	A0839814 260L13-C5
9	366.6	25.4	839	9	AV700988	AV700988 AV700988
10	360	25.0	1148	9	AV761207	AV761207 AV761207
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12	358.8	24.9	687	12	AG186062	AG186062 Pan trogl
13	357.8	24.8	679	10	BF346320	BF346320 602018525
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16	355.4	24.6	1808	11	BC017826	BC017826 Homo sapi
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ALIGNMENTS

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VERSION BC011119.1 GI:15029795
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1842)
Strausberg, R.
Direct Submission
Submitted (25-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA

REMARK
COMMENT
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNU)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalob@bcm.tmc.edu
Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNU at: <http://image.llnl.gov>
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Db	966	GCGTGGCCTCTTTTTTTTTTTTGGAGATGA-----ATCTCCCTCTGTACCCAGATTGG	1038
QY	479	agtgcaatggtgtgatacacaagctcaact-----gcagctcttaac	517
Db	1039	ACTGTAGTGGTGCATCTCAGCTCAGCTCAGCAACTCGGGTAGTTGCCAGGCCAATCTCCG	1099
QY	518	tctgaagatcaagc-alcctcctcgtccacagctcccaagtagctgagaccaagaatgc	576
Db	1099	TCTGGGTTCAAGCAATTTCTCTGCTCCACACCTCCGAGTAGCTGAGTTTACAGGCGAT	1158
QY	577	accactaacctgtgctaattttttttttaattttttaatttttgagacaagagctcaact	636
Db	1159	GCCACACAGCGCTGGCTAATTTTGTGTTTTTTTTTTTGAAGACAGTCTCT--CT	1215
QY	637	ctgtgacacagggctgagagtgacatgctgcaactttggtctactgtcaacctgtgctccg	696
Db	1216	CTGTCA-CCAGGCTGGAGTCAAGTGCAGATCTTGCGTCACTGTCAACCTCGCTCCCG	1274
QY	697	ggttcaagtattctcctgcccagcctcctgagtagctggtggaactacagagcgcccaac	756
Db	1275	GGTTCAGCGCATTTCTCTG-GCCAGCTCTCAAGTAGCTGGGACTACAGGCCGCCGCCAC	1333
QY	757	ggctagctaatt-ttttttgtatttttaagtagagatgggg-ttacccaatgtgcgccaagt	814
Db	1334	CATGCCCGGCTAATTTTTGTATTTTATAGTAAGAGTGGGGTTTACACATGTTGGCAGAT	1393
QY	815	gattctatctcgagacctgtgatatctgcctgcctccgcgcctccaagtgctgattac	874
Db	1394	GGTCTAAATCTGTGACCTCATGATTCACCCACTCTCAGCTCTCCAAATGCTGGGATTAAC	1453

[illegible]

RESULT	2
A0739838/c	
LOCUS	A0739838
DEFINITION	877 bp DNA linear GSS 16-JUL-1999 HS-5505-A1-C09-T7A RPCI-11 Human Male BAC Library Homo sapiens
ACCESSION	A0739838
VERSION	A0739838
KEYWORDS	Genomic clone Plate=1081 Col=17 Row=E, DNA sequence.
SOURCE	GSS.
ORGANISM	Homo sapiens

REFERENCE
1 (bases 1 to 877)
AUTHORS
Mahabir, G. G., Wallace, I. C., Smith, K., Gurevitz, O.,
Lunay, J., Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE Sequence-tagged connectors: A sequence approach to mapping and

JOURNAL
MEDLINE
COMMENT
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
Contact: Mahairas GG, Wallace TC, Hood L

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: +1 206 616 8888

Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human PAC library pB7-11

For further availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from National Gene Bank (<http://www.ngb.org>).

http://www.htsc.washington.edu
plate: 1081 row: E column: 17
Seq primer: T7

source	Class: PAC ends	High quality sequence stop: 877.	Location/Qualifiers
1	877		

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/organism="Homo sapiens"  
/db_xref="taxon:9606"  
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/closure_id="rfci-11 Human male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated as follows"

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and partially digested with a combination of *EcoRI* and *EcoRI* Methylase. Size selected DNA was cloned into the pBACe3.6 vector at *EcoRI* sites"

ORIGIN	204 3	101 0	442 9	203 7
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100				

Query Match	27.1%;	Score 391.4;	DB 12;	Length 877;
Best Local Similarity	79.4%;	Pred. No. 2.3e-76;		
Matches 514; Conservative	0;	Mismatches 126;	Indels 7;	Gaps 4;

568 aagacatgcaccactacacccgtgctaattttattttatttttaatttttgagacaga 627

OY	1141	gaccacctctcgcacgtcccaaaagtcggcgattacaaggcttgacacccaccacc	1200
Db	3678	GATCGACTGCTCAGCTCCACAAATGTGGATTACAGGCGTGAACCAACACCACCGG	3737
OY	1201	cc 1202	
Db	3738	CC 3739	
RESULT	9		
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LOCUS	AV700988 GK C Homo sapiens cDNA clone GKCAEA01 3', mRNA sequence.		
DEFINITION	AV700988		
ACCESSION	AY700988		
VERSION	AV700988.1	GI:10302959	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 839)		
AUTHORS	Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,Y., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.		
TITLE	Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of liver hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)		
JOURNAL MEDLINE COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Gene Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel.: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzge@chc.sh.cn This clone is available at CHGC in Shanghai.		
FEATURES	Location/Qualifiers		
source	1..839		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
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	/clone_1ib="GKC"		
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	/dev_stage="Adult"		
	/lab_host="SOLR"		
	/note="vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"		
PAGE COUNT	144 a 259 c 203 g 231 t 2 others		
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Query Match	25.4%; Score 366.6; DB 9; Length 839;		
Best Local Similarity	81.4%; Pred. No. 7e-71;		
Matches	499; Conservative 0; Mismatches 101; Indels 13; Gaps 6.		
OY	602	ttttattttaatttttttagagacagatctcaactctgcacacagcgctggagttagt	661
Db	66	TTCCTTTTTTTAATTTTTTAAGCAGGAGCT-GGCTTGTCACCCAGCTGGAGATGCAAGC	124
OY	662	ggcacatcttgtgctaactgaacacctgctcccgggtccaagtlacttctgtccccag	721
Db	125	GCGCGATCTGGCTACTGAAAGCTCTTCTCTCCCGGGTTCAACCCATTCTCGCTCAA	184
OY	722	cctctcgtagtagctgggactacagcg---ccaccaagcctagcataattttttgtatt	778
Db	185	CCGCCGAGTAGCTGTGAATATACAGGGGTTGCCACCAAGCCAGCATTAATTTTTGTATT	244
OY	779	tttagtagaatatggg--ttaccabtgctcccaaggttgatcatctgacaccttgag	837
Db	245	TTTAGTAGAACAGGGGTTTACCGGTGTATACCAAGATGCTGTGAACTCTCTGACTCGTG	304

QY	838	atctgcgtcgtcgtgcctcccaaaatgcttggttgattacaaggcgtgagccacacagcgccgc	897
Db	305	ATTCGCTCGCTCGGCGCTCCCAAGTCTGGATTACAGGCTTGAGCCACGCCACCGCCGG	364
QY	898	ttattcttaattttgttttttttgtaaatggaatctcaactctgttaccaggctgtagtc	957
Db	365	CTCTATTATTTTTTTT-----TTTGAGATGAGTCTCATCTGTCACCTCGGGCTGAGTGC	418
QY	958	aatgagcaaatctcgtcgtcaactgcaactctgctcccggtcccaagcagttctctgtc	1017
Db	419	AGTGAAGAGATCTCGGCTCATCTGCACCTCGMCTCTGTGGTTCAAGATTCCTCGCC	478
QY	1018	tcagacc-tcccaagcagctggtgattacgggaacctgcccacaacaccccgcta-attttg	1075
Db	479	TCAGCCTTTCCAAATAGCTGGGATTTACAGTGCCCGCACACAGCCCTGGGTAGTTTTTG	538
QY	1076	tatttcattagagcggggtttcacatatattgtcagcgtgctcctaactcctgacct	1135
Db	539	TATTTTATGGCAAAATGGGGTTTACATGCTGCGCAGGCTGTTCCTTGAACTCTTGACAT	598
QY	1136	caggtgaccaccccgccctcacaccttccaaagtctgttgattacagcgctgagccacta	1195
Db	599	CAGGTGAACCCGCCCACTTAAGTCTCCAAAGTGTGGGATTACAGGCTGAGCCACCATTA	658
QY	1196	cccaagcgagctca 1208	
Db	659	CCTGGCGCCGCAAAA 671	
RESULT 10			
AV761207/c		1148 bp	linear
LOCUS	AV761207		EST 19-OCT-2000
DEFINITION	AV761207 MDS Homo sapiens CDNA clone MDSBZH05 5', mRNA sequence.		
ACCESSION	AV761207		
VERSION	AV761207.1	GI:10919055	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 1148)		
AUTHORS	Gu,Y., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Zhang,Q., Chen,S., Han,Z. and Chen,Z.		
TITLE	Homo sapiens CDNA MDS clones		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Email: hanzg@hgc.sh.cn This clone is available at CHGC in Shanghai.		
FEATURES			
source	Location/Qualifiers		
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	/db_xref="taxon:9606"		
	/clone="MDSBZH05"		
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	/tissue_type="Bone marrow"		
	/cell_type="CD34+ hematopoietic stem/progenitor cell"		
	/lab_host="PM25.8"		
	/note="Vector: pTRipleX2; Site_1: sfIra; Site_2: sfIIP"		
BASE COUNT	328 a 271 c 291 g 249 t		9 others
ORIGIN			
Query Match	25.0%	Score 360;	DB 9; Length 1148;
Best Local Similarity	80.9%	Pred. No. 1,9e-69;	
Matches 491; Conservative	0;	Mismatches 99;	Indels 17; Gaps 6;

OY	599	tatttttattttaatttttttgagacagagtctcaactcgtaccaaggctgtagtga	658
Db	608	TTTTTNTTTTNTTTTNTTTTGTGAGACCACTC-ACCTGTGCCCCAGCGTAGAATGA	550
OY	659	gtggcgcaatctggtctcaactcacctctgcctccgggttaagtatttcctccc	718
Db	549	GTCGGCGNATCTCAGCTCACACTGCACACTCTGCTCTNNGGGTTACAGCAATTCTTGCCC	490
OY	719	-cagctccctgaatagctggaactaacaggcgccccaccagcctaagtaat-tttttgta	776
Db	489	TCAAGCTCTGAAATTAAGTCTGGGATAAGGGGNCOCGANNACNGCCAGCTAATTTTGTGA	430
OY	777	tttttagtagaga-tggsgttcaccaatgttcgcgaagttatctgaatctctgacctg	835
Db	429	TTTTTAGTAGAGACAGGGTTCATCATGTTGGCCAGGCTGTCTTGAATCTTGACCTCG	370
OY	836	tgatctgctgctctggtcctcccaaagtctgtagattacaaggcgtgagccacagccg	895
Db	369	TGATCCACCACCCACGCGACTCCCAAGTGTGTGGATTACAGGGCGTGAGCCACCATCGCCG	310
OY	896	gc-----ttaatttaattttgttttttgaatgaatcctcatcctgttac	944
Db	309	GCCTCATTTGGCACTCTTTTTTTTTTTTTTTTTTTCTTTTGAGATGAGTCTCACTCATTTAGCC	250
OY	945	caggctcgtagtgtcaatgagccaatctcggctcaactgcaactctgctcccggtctaa	1004
Db	249	CAGGCTGGAGTCTGTGGACAATCTCGGCTCACTCACTCAACTCTGCTCCGGAATCAAG	190
OY	1005	cgattcctgtctcaagctcccaagcagctggaattgaagggaactcgcacccaacccc	1064
Db	189	TGATTCCTCTGCCTCAGCCTTCOGAATACTGGGATTACAGCATACACACCATTCGCCA	130
OY	1065	gctaatatttgtaatttcattagaggcggggtttcaacatatlttgcaggtgtgtccaa	1124
Db	129	GCTAATTTTGTATTTTACTAGAGACAGGCTTCCACCACATGTGGTGAAGCTGTCTCAA	70
OY	1125	actctgacctaaagtggaccacactcgcctccagcttccaaaagtgtcgggattacaagggt	1184
Db	69	ACTCCTGACCTC-GTGANCCGCCGCCCTCAGCCTCCCAAGAAGTGTCTGGATTACAGGCGT	12
OY	1185	gagccac 1191	
Db	11	GAACAC 5	
RESULT 11			
AGI50197/c			
LOCUS			
DEFINITION	AGI50197 667 bp DNA linear GSS 09-JAN-2002		
KEYWORDS	Pan troglodytes DNA, clone: RP43-012023.T7, genomic survey sequence.		
ACCESSION	AGI50197		
VERSION	AGI50197.1 GI:16679875		
SOURCE	GSS: GSS (genome survey sequence). Pan troglodytes male lymphocytes DNA, clone_1lb:RPCT-43 Chimpanzee Male BAC library clone:RP43-012023.T7.		
ORGANISM	Pan troglodytes		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.		
AUTHORS	1 (sites)		
TITLE	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.		
JOURNAL	BAC end sequences of Library RPCT-43 unpublished 2 (bases 1 to 667)		
REFERENCE	Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.		
AUTHORS	Direct Submission Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chinpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)		

	COMMENT	Clones are derived from the chimpanzee BAC library RPI-43 This BAC was generated during the Rad process and may have higher chance of clone tracking errors.					
	PRIMERS	Sequencing: T7					
	LIBRARY	Vector : PBACE3.6 R.Site 1 : EcoRI R.Site 2 : EcoRI. Location/Qualifiers 1..667					
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	BASE COUNT	192 a	163 c	184 g	128 t		
	ORIGIN						
QY	Query Match	25.0%;	Score 359.8;	DB 12;	Length 667;		
Db	Best Local Similarity	81.3%;	Pred. No. 2.3e-69;				
Matches	495; Conservative	0;	Mismatches 97;	Indels 17;	Gaps 6;		
QY	601	tttattatattaaatttttagagacagagtctcaactgttcaccacgagcttgagt----	656				
Db	659	TTTTTTTATTTTTTTTTTTTGAGACAGAGCT-TGCTGTCTCCAGCGGTGGAGTACAGN	601				
QY	657	cagtcggcgaactcttgctcactgcataacctctgctccgggtltaagtattctctcg	716				
Db	600	CAGTGGAATCGAATGTCGGCTCACTGCCACTCCACCCTCCAGGTGCAGCATTCTCTCG	541				
QY	717	cccagcctccagtagtgtgagactagaggggccccacagcctagc--taattttttg	774				
Db	540	CTGGGCTCCCAAATAGCTGGGATTACAGGGCCCCAACACACGACCTAATTTTGG	481				
QY	775	tattttaagtagagatggg-ttacaccaftctgcagaagtgtatcttgcctgacct	833				
Db	480	TATTTTAGTAGAGACAGCGGGTTTCACATGTATTAGCCAGAGATGCTCGATCTCTGACT	421				
QY	834	tgtgatctgctgctcggcctcccaaagtctgagattacaagcgltgagccaacgccc	893				
Db	420	TGTGATCCACCCGCTCTGGCCTCCCAAAGTCTGGGATTACAGCATAGCACCGCTGC	361				
QY	894	cggactaatltaaattttgtttgtttgtaaaatggaatctcaactcgtltaaccaggtga	953				
Db	360	TGGCTT-----TTTTTTTTTTTTTAAGACAGAGTTTGTGCTTGTTGCCAGGCTGSA	308				
QY	954	gtccaatggccaatatcgcgctcacctcaactcgtctcccggtctcaagcgattctcc	1013				
Db	307	GTCGAATGGCGCATCTCAAGTCTCACTGACGTGAACTCTGCTCCCGGTTAAAGGATTTGCC	248				
QY	1014	tgtctaagcctcccaaagcaagtgtatctagcggcaacctgccaaccaaaccccgtaattt	1073				
Db	247	TGCGCTCAGCCTCCTGAGTACTGTGGATTACAGCATGTGACACATGCTGTGGCTAATTTT	188				
QY	1074	tgtattttaatttaaggagcgagggtttaccatatattgtcagagctgtgtctcaactctgac	1133				
Db	187	TGTAATTTTAAAGTAGAGCGGGGTTTACCAATGTTGTGTCAGGCTGCTCGAAATCTCTAAC	128				
QY	1134	ctcaagtlgacccaactgtcctccacagcctcccaaagtgtctgaggtltaagcgltgagccact	1193				
Db	127	CTC--GTGATCCCGCTGCGCTCAGCGCTCCAAAAGTGTGGGATTACAGCGGTGAGACACCA	70				
QY	1194	caccagcg 1202					
Db	69	TGCCCAAGCC 61					
RESULT 12							
AG186062/c							
LOCUS	AG186062	587 bp	DNA	FASTA	589.00	199.00	0.00

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DEFINITION Pan troglodytes DNA, clone: RP43-060F11.T7, genomic survey
SEQUENCE
AG186062
AG186062.1 GI:16715742
GSS: GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone: lib.RPCI-43 Chimpanzee
Male BAC Library clone: RP43-060F11.T7.
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library RPCI-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 687)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Aaso Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpbes@sc.riken.go.jp, URL: http://hpg.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES
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location/Qualifiers
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/clone="RP43-060F11.T7"
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BASE COUNT 207 a 161 c 182 g 137 t
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Query Match 24.9%; Score 358.8; DB 12; Length 687;
Best Local Similarity 81.2%; Pred. No. 3.8e-69;
Matches 492; Conservative 0; Mismatches 102; Indels 12; Gaps 6;

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QY 958 aatggccaatctcgctcaactgcaacccctgctcccggtcaagcattctctg 1017
DB 301 AATGGCGCAATCTCAGCTCAGTGCACACCTCTGCTCCGGTTCAAGATGTCTCGC 242
QY 1018 tcaagctcccaacgaactggaattacgggcaactgcccacaccccgtaatttga 1077
DB 241 TCAGCCTTCAGTACCTGGATTCAGGACGACGACGACGACGACGACGACGACG 182
QY 1078 ttctaatgaagcggggtttacacattttcagg-ctggtctcaactctgaccc 1136
DB 181 TTTTGTAGTAGAGAGGGGTTTACCAATGTTGGTCAGGACTGTTCTGAACCTTAAC 122
QY 1137 aggtgaccaccccgctcgaactcgaactggaattacagcgctgagcgaactcac 1196
DB 121 A--TGATCCCGCTCGCTCAGCCCTCCCAAGTGTGGATTACAGGTGATGACCATGC 64
QY 1197 ccagcc 1202
DB 63 CCAGCC 58
RESULT 13
BF346320/c 679 bp mRNA linear EST 22-NOV-2000
LOCUS 602018525F1 NCI_CGAP_Brn67 Homo sapiens CDNA clone IMAGE:415399
DEFINITION 5', mRNA sequence.
ACCESSION BF346320
VERSION BF346320.1 GI:11293915
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs@remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
plate: L1AM9423 row: a column: 08
High quality sequence stop: 661.
FEATURES
source
location/Qualifiers
1..679
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/db_xref="taxon:9606"
/clone="IMAGE:415399"
/clone_lib="NCI_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with 1p/19q
loss"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: brain; Vector: PCMV-SpRTE; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 200 a 161 c 191 g 127 t
ORIGIN
Query Match 24.8%; Score 357.8; DB 10; Length 679;
Best Local Similarity 79.9%; Pred. No. 6.3e-69;
Matches 485; Conservative 0; Mismatches 112; Indels 10; Gaps 5;
QY 600 atttatttatttatttggagagagctcaactctgtacccagcgctggagtgag 659
DB 676 ATCTCTTGTCTTCGCTATTTGAGAGGAGTGTGCTCTGTGTGCCACGCTGAGTGCAG 617

```


Thu Apr 25 08:07:06 2002

us-09-964-678a-1.rst

Page 12

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 18:39:56 ; Search time 207.25 Seconds
(without alignments)
11945.914 Million cell updates/sec

Title: US-09-964-678A-1
Perfect score: 1442
Sequence: 1 ttttttttttgcagatgagag.....ttaacaacagcttagagca 1442

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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24: /SIDSL/gcgdata/hold-geneseq/geneqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1223.4	84.8	1418	17	AAT27738
2	1078.6	74.8	1381	15	AAQ77883
3	1077	74.7	1381	17	AAT27765
4	517.2	35.9	33747	22	AAK69279
5	517.2	35.9	33747	22	AAK73093
6	511.6	33.5	5262	22	AAK71768
7	511.6	33.5	5262	22	AAK71769
8	489.6	34.0	24167	22	ABA16132
9	478.2	33.2	31853	22	AA198993

C	10	478.2	33.2	31853	22	AA16343	Human kidney relat
C	11	477.4	33.1	11319	22	AA53682	Genomic sequence #
C	12	477.4	33.1	11319	22	AAK90025	Human digestive sy
C	13	475.4	33.0	14796	19	AAV27941	Survivin gene. Ho
C	14	475.4	33.0	14796	22	AA52123	DNA encoding human
C	15	475.4	33.0	14796	22	AAH47531	Human Her-3 genom
C	16	471.2	32.7	12542	22	AA526800	Human genomic DNA
C	17	467	32.4	15041	22	AA535921	Human cardiovascular
C	18	466.8	32.4	9236	22	AA503689	Rhesus gene locus:
C	19	466.8	32.4	9236	22	AA503690	Rhesus gene locus:
C	20	466.8	32.4	9236	22	AA503688	Rhesus gene locus:
C	21	461.8	32.0	12026	22	AAK67211	Human immune/haema
C	22	461.4	32.0	36221	22	AA500624	Human death-associ
C	23	460.8	32.0	2368	22	AAK69566	Human immune/haema
C	24	459.4	31.9	30110	22	AAK69230	Human digestive sy
C	25	457.8	31.7	160552	22	AAK62697	Human glycosyl sul
C	26	457.4	31.7	38771	22	AAK81036	Human immune/haema
C	27	456.4	31.7	16310	21	AAK21086	Human low adenosin
C	28	456.4	31.7	16310	21	AAK4964	Human low adenosin
C	29	456.4	31.7	17634	21	AAK21087	Human immune/haema
C	30	456.4	31.7	17634	21	AAK34965	Human immune/haema
C	31	456.2	31.6	23130	22	AAK77045	Human immune/haema
C	32	455.2	31.6	44354	22	AAK77833	Human immune/haema
C	33	455.2	31.6	44354	22	AAK77836	Human immune/haema
C	34	455.2	31.6	44354	22	AAK77837	Human immune/haema
C	35	455	31.6	17245	22	AAK83897	Human AKAP10 gene
C	36	455	31.6	161425	22	AAH02340	Human AKAP10 gene
C	37	455	31.6	162025	22	AAH02339	Human AKAP10 gene
C	38	452.6	31.4	13161	22	AAK7867	Human neuroblastom
C	39	452.2	31.4	4077	22	AAK69603	Human immune/haema
C	40	452.2	31.4	4077	22	AAK69605	Human immune/haema
C	41	452.2	31.4	10091	22	AAK69350	Human immune/haema
C	42	450	31.2	21693	22	AAK79930	Human immune/haema
C	43	449.4	31.2	1235	22	AAK87086	Human immune/haema
C	44	448.6	31.1	15745	22	AAK79250	Human immune/haema
C	45	448.4	31.1	16707	20	AAK38061	Genomic DNA for Hu

ALIGNMENTS

RESULT 1	AA27738	standard; DNA; 1418 BP.
ID	AA27738	
XX	AA27738;	
AC	13-NOV-1996	(first entry)
DT	Neural thread protein coding sequence.	
XX	Neural thread protein; NTP; diagnosis; detection;	
XX	Alzheimer's disease; neuroectodermal tumour; malignant astrocytoma;	
KW	monoclonal antibody; binding fragment; ds.	
KW	Homo sapiens.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	14..1207
FT		/tag= a
FT		/product= Neural thread protein.
PN	W09615272-A1.	
PD	23-MAY-1996.	
XX	14-NOV-1995;	95WO-US17111.
XX	14-NOV-1994;	94US-0340426.
XX	(GEHO) GEN HOSPITAL CORP.	
PA	De LA MONTE S,	Wands JR;
XX		
PI		

XX WPI; 1996-259865/26.
 DR P-PSDB; AAR95913.
 XX
 PT Detection of neural thread protein in diagnosis of Alzheimer's
 PT disease - also NTP DNA and protein sequences used in gene and
 PT anti-sense therapy
 XX
 PS
 XX
 PS Claim 24; Page 168-170; 238pp; English.
 CC A method for detecting the presence of neural thread protein (NTP)
 CC having a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human
 CC subject comprises (a) contacting a sample from a human subject that
 CC is suspected of containing the NTP with at least one molecule
 CC capable of binding to the protein; and (b) detecting any of the
 CC molecule bound to the protein. The binding molecule is selected
 CC from an antibody free of natural impurities, a monoclonal antibody
 CC or a binding fragment of either of these. The method may be used for
 CC diagnosing the presence of Alzheimer's disease, neuroectodermal
 CC tumours and a malignant astrocytoma in a human.
 SO Sequence 1418 BP; 302 A; 396 C; 315 G; 405 T; 0 other;

Query Match 84.8%; Score 1223.4; DB 17; Length 1418;
 Best Local Similarity 96.9%; Pred. No. 0;
 Matches 1375; Conservative 0; Mismatches 31; Indels 13; Gaps 12;

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 DB 1 ttttttttgaagatgagtttgcctctgttgcctcaggctgagtgcaatggcgaat 60

QY 62 ctcaagctacccgaacacccctccgctccgggttcaagcattctccctcagccctccc 121
 DB 61 ctcaagctacccgaacacccctccgctccgggttcaagcattctccctcagccctccc 120

QY 122 agta-gctggatctacagcatgtgcaaccacgcctcggttaatttggat 180
 DB 121 agtagctggtgattacagcatgtgca-ccagctcgcgttaatttggat 179

QY 181 tagagtgagtttctccatgtgtgcagctgtgtctcgaactcccgactcaatgatc 240
 DB 180 tagagtgagtttctccatgtgtgcagctgtgtctcgaactcccgactcaatgatc 238

QY 241 cctccgctcgcgctcccaagtgctagatacagagctgagccatgcccgcg-ctctgc 239
 DB 239 cctccgctcgcgctcccaagtgctagatacagagctgagccatgcccgcg-ctctgc 238

QY 300 ctgagctaattttgtgtgtagaacaaggtttcaactgtgccaagctggtctcctgag 359
 DB 299 ctgagctaattttgtgtgtagaacaaggtttcaactgtgccaagctggtctcctgag 358

QY 360 ctcaagcagctcagctcctcagccctcccaagtgctgtagatcaagggctgagccgtg 419
 DB 359 ctcaagcagctcagctcctcagccctcccaagtgctgtagatcaagggctgagccgtg 418

QY 420 cctgagccttttatttatttttttaagacacaggtgtcccaactcttcccaagatgaa 479
 DB 419 cctgagccttttatttatttttttaagacacaggtgtcccaactcttcccaagatgaa 478

QY 480 gtgagtggtgtgtagacagctcagctcagcttcaactcccgatgaatcaagatcctct 539
 DB 479 gtgagtggtgtgtagacagctcagctcagcttcaactcccgatgaatcaagatcctct 537

QY 540 gctcagcctccc-aagtagctgagcaacaagacatgacccactacactgtgctaat 598
 DB 538 gctcagcctccc-aagtagctgagcaacaagacatgacccactacactgtgctaat 597

QY 599 tatttttttttaatttttttttgaagacagatctcaactgtgccaagctgagtgca 658
 DB 598 tatttttttttaatttttttttgaagacagatctcaactgtgccaagctgagtgca 657

QY 659 gtgagcgaactgtgctcaactgcaacccctgctccgggttcaagtatttctcctgcc 718

DB 658 gtgagcgaactgtgctcaactgcaacccctgctccgggttcaagtatttctcctgcc 717

QY 719 cagcctcctgagtagctgtagctacagcgcccaacagcctgaatttttttatt 778
 DB 718 cagcctcctgagtagctgtagctacagcgcccaacagcctgaatttttttatt 777

QY 779 tttagtagagatggg-ttccacatgttcgcaagtttag-ctgatatctgagactgt 836
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 DB 838 gattgtcgtcctgagcctcccaagatgctgagttacag-cgttagccaacagccgcg 897

QY 896 gctatttttattttgtttgttgaatggaattcgaactctgttccagagtgag 955
 DB 898 gctatttttattttgtttgttgaatggaattcgaactctgttccagagtgag 957

QY 956 gcaatggccaatctcgctcaactgcaacactctgctcccggtcgaagcgtatctctg 1015
 DB 958 gcaatggccaatctcgctcaactgcaacactctgctcccggtcgaagcgtatctctg 1017

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 DB 1018 tctcagcctcccaagcagctgggattagcgggcaactg-caacaccccgtaattttg 1076

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QY 1136 caggtgacccaactgctcgaactcccaagatgctgagattacagcgctgagccaactca 1195
 DB 1137 caggtgacccaactgctcgaactcccaagatgctgagattacagcgctgag--cgctca 1194

QY 1196 ccagcggcgttaatttagataaaaaaatatgtagcaatgggggtctgttatgtggcc 1255
 DB 1195 ccagcggcgttaatttagataaaaaaatatgtagcaatgggggtctgttatgtggcc 1254

QY 1256 aggcgtgtctcaactctgtgtctcatgcaatcctcccaatgagccaacacccagcc 1315
 DB 1255 aggcgtgtctcaactctgtgtctcatgcaatcctcccaatgagccaacacccagcc 1314

QY 1316 agtcaattttttaaacagttacatcttatttttagtatactagaagaataataa 1375
 DB 1315 agtcaaca-tttttaaacagttacatcttatttttagtatactagaagaatgataa 1373

QY 1376 catgtcaaacctgcaaatcagtagtaacagagttctt 1414
 DB 1374 atgagcggaacctgcaaatcagtagtagtaacagagttctt 1412

RESULT 2
 AAQ77883
 ID AAQ77883 standard; cDNA; 1381 BP.
 XX
 AC AAQ77883;
 XX
 DT 06-JUL-1995 (first entry)
 XX
 DE Neural thread protein AD10-7 cDNA.
 XX
 KW Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours;
 XX malignant astrocytomas; glioblastomas; ss.
 OS Rattus rattus.
 XX
 PN WO9423756-A.
 XX
 PD 27-OCT-1994.
 XX
 PF 20-APR-1994; 94WO-US04321.
 XX

RR	20-APR-1993:	93US-0050559.
XX	(GEHO) GEN HOSPITAL CORP.	
FA		
XX	De LA MONTE SM, Mands JR;	
PI		
XX	WPI, 1994-341497/42.	
DR		
XX	Detection of neural thread proteins - to detect sporadic and	
PT	familial Alzheimer's disease, neuroectodermal tumours, malignant	
XX	astrocytomas and glioblastomas (Eng).	
XX		
PS	Example 4; Fig 16R; 158bp; English.	
XX		
CC	AA077883 is the AD10-7 neural thread protein (NTP) cDNA. This	
CC	sequence was used in the development of an antibody dependent	
CC	method, for the detection of NTPs. This new method could be	
CC	used to diagnose Alzheimer's disease (differentiating between	
CC	sporadic and familial), neuroectodermal tumours, malignant	
XX	astrocytomas and glioblastomas.	
XX		
SO	Sequence 1381 BP: 296 A: 385 C: 301 G: 399 T: 0 other;	
Query Match		
Best Local Similarity 74.8%; Score 1078.6; DB 15; Length 1381;		
Matches 1316; Conservative 0; Mismatches 54; Indels 25; Gaps 18		
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QY	62 ctacagtcacgcgaacatctccgctccgggttcaagagatctctgctcagctccc 121	
DB	61 ctacagtcacgcgaacatctccgctccgggttcaagagatctctgctcagctccc 120	
QY	122 agtacctgggattacagagatgagccacagctggcattttgatttttttagt 181	
DB	121 agtacctgggattacagagatgagccacagctggcattttgatttttttagt 179	
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QY	240 ccctcgctcgcgcctcccaaatgtct--agatacagagactggccacatgcccgt 295	
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DB	300 ctgacctgccaattttgtgtgtagaacaaggtttcactatg--tgccaaagctgtgtc 359	
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DB	360 ctgacctgaacagatccacactgtcctcagcctcccaaatgtctgagattacagcggtcag 418	
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QY	475 atgaagtgcagtgtgtatatacagctcactgtcagccttcaactctgataatcaagc 533	
DB	479 atgaagtgcagtgtgtatatacagctcactgtcagccttcaactctgataatcaagc 538	
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DB	598 attttattttatttttaatttttttgagacagagttc--actcgttaccacaaagcttga 656	
QY	654 gtgcagtgccgaactctgtcactcagactcgtcctccgggttcaagtattatctcc 713	

Db	657	gtgcagctgacgaaccccttgagctcaacgaacctcgctcccggttccaagtattctcc	716
QY	714	tgccccagcctcctctgagtagcttggactacagcgccacacagcctagactaattttt	773
Db	717	tgccccagcctcctctgagtagcttggagctaacagcgccacacagcctagactaattttt	776
QY	774	gtatttttaagaagatggg--ttcacatgcttcgcagagttgaattcttgactcttgacc	832
Db	777	gtatttttaagaagatgggttttcaacatgcttcgcagagttgaattcttgactcttgacc	836
QY	833	tttgactctgcctcgccctcgccct--cccagaagtcgaggatatacagcgctgaagccacag	891
Db	837	tttgactctgcctcgccctcgccctccacccaagatgctcgaggattacag--gtcgtgactcac	894
QY	892	cccggtatttttaatttttgtttgttttgaatggatcttcactctgtttaccaggtg	951
Db	895	gcgcgcctatttttaatttttgtttgtttgaatggaaactcaactctgtataccaggtcg	954
QY	952	gagtgcaatgccaacatctcgctcgaactgcaacactgctgcctcccggtgtcaagcattct	1011
Db	955	gagtgcaatg--caaatctcgctactcgaacactctgctctccggg--tcaagcgattct	1012
QY	1012	cctgtctcagcctcccaagcagcttggatlaegggcacctgccaacacaccccgctaat	1071
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Db	1129	gaccctcaggtgacccaacactgctcagccttccaaagtctgtggatttaacagcgtagacca	1188
QY	1191	ccttaccacagccggcttaattagttaaanaaatatgtagaatctggggggtctgtcatgt	1250
Db	1189	ccttaccacagccggcttaatttggaaataaataatgtagaatggggg--tctgtcatgt	1246
QY	1251	tgccccagctgtgtccaactctcgcttcaatgcaatccttccaaatgagccacaacac	1310
Db	1247	tgccccagctgtgtccaactctcgcttcaatgcaatccttccaaatgagccacaacac	1306
QY	1311	cagccagctcaattttttaacagttacatcttattattagttatcactagaagaattatac	1370
Db	1307	cagccagctcaattttttaacagttacatcttattattagttatcactagaagaattatac	1366
QY	1371	atnaacatgtcaaac	1385
Db	1367	ataaacatgtcaaac	1381
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AAT27765			
ID	AAT27765	standard; cDNA; 1381 BP.	
AC	AAT27765;		
XX	14-NOV-1996 (first entry)		
DT			
XX	AD 10-7 human neural thread protein clone (partial sequence).		
DE			
XX	Neural thread protein; NTP; diagnosis; detection;		
KW	Alzheimer's disease; neuroectodermal tumour; malignant astrocytoma;		
KW	monoclonal antibody; binding fragment; ds.		
XX			
OS	Homo sapiens.		
XX	WO9615272-A1.		
PN	23-MAY-1996.		
XX			
PF	14-NOV-1995;	95WO-US17111.	

OS Homo sapiens.
XX WO200157182-A2.
XX
PD 09-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01354.
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31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
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PR 11-JUL-2000; 2000US-0217487.
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PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
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PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
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PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
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CC amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
CC activity, and can be used in gene therapy, and vaccine production. (1)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (1) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (1) by expressing inactive proteins or to
CC supplement the patient's own production of (1). Additionally, (1)
CC polynucleotides may be used to produce the secreted (1), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (1) proteins and polynucleotides may be used to prevent,
CC diagnose and treat metastases/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK35950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
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 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPL: 2001-483426/52.
 Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 useful for preventing, diagnosing and/or treating cancers and
 metastasis -
 PS Disclosure: SFO ID NO 26580; 3071pp + Sequence Listing; English.
 PS
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM62170 to AAM91921. (I) have cytosolic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially

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 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483426/52.
 DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Disclosure: SEQ ID NO 26581; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 5262 BP; 1100 A; 1346 C; 1245 G; 1571 T; 0 other;

PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226686.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0231415.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234224.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 25-SEP-2000; 2000US-0234999.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235634.
 PR 27-SEP-2000; 2000US-0235635.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239335.
 PR 13-OCT-2000; 2000US-0239337.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 20-OCT-2000; 2000US-0242221.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246532.

PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249219.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250391.
 PR 01-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-541565/60.
 DR Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 XX useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 PS
 PS Disclosure; SEQ ID NO 8463; 1701bp + Sequence Listing; English.
 XX
 XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABA14678-AB18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WPI at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SO Sequence 24167 BP; 6223 A; 6198 C; 6379 G; 5367 T; 0 other;

Query Match 34.08; Score 489.6; DB 22; Length 24167;
 Best Local Similarity 69.8%; Pred. No. 4.3e-120;

Dh 3149 TCTGGCTCAGTCAACCTCCACCTCCGGGTTCAAGTATGATTTCCCATGCTCAGCCTC 3090
Qy 119 cccagtagctggagatatacaggaatgacacccagcctcgcttaatttgaattttttt 178
Dh 3089 CCGATAGTACGTGGGATTAATAGTTGCGTGCCACACACCTGGCTAATTTT---TGATATTTT 3033
Qy 179 agtagagatggagattctcactgltgtagcagctggtctcgaactcccgacctgaatga 238
Dh 3032 AGTAGAAGAGGGGTTTACACCATGTTGGCCAGGCT-GTCTTGAACTCCTGACCTAGGTGA 2974
Qy 239 tccccgtctcgacctcccaagtgctag---atacagactggccacatgcccgcg 294
Dh 2973 TCCACCTGCTTGGGCTCCCAAGTCTGGATTAACAGGGGTGAGCCAGCCGCGAGCT 2914
Qy 295 tctgcctggcctaatttggtagaagagggttcactagatggtcccaagctggtctc 354
Dh 2913 AATAAATAATTAATTAATTTTGGAGACGAGTCTGCTCTGCGCCAGCGCGGAGCTG 2854
Qy 335 ctgagctcaagcagctcactgctcagcctcccaagtgctgagattacagcggtgag 414
Dh 2853 CGGA----CTGCAAGTGGCCCAATCTGGGCTCACTGCAAGTCCGCTCCGGGTTCAAGC 2798
Qy 415 ccggtccggtccttttatttatttattttaaagacaggtgtccactcttaaccag 474
Dh 2797 CATTCCTGCTCAGCCCTCAGTACGCTGGGACTGAGGCGCCGCGCCAGCCGCGCGG 2738
Qy 475 atgaagtgcaagtgtgtagatcacag-----ctcactgcagccttca 515
Dh 2737 CTAAATTTTGTATTTTATAGTAGAGAGCGGGTTTACCTTTGTTAGCCAGAGTGTCTCGA 2678
Qy 516 actctgagatcaagcactcctcctcagcctcccaagtagctggagacaaagacatg 575
Dh 2677 TCTCTGTACACTCATG-ATCCACCCGCGCTCGGCTCCCAAGTCTGGGATTAACAGGCGTG 2619
Qy 576 caccactacactgcttaatttatttatttatttatttatttgaagacagagctccaac 635
Dh 2618 AGCCACCGCGCCAGC-----CTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 2568
Qy 636 tctgtcacccagctgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 695
Dh 2567 TCTGTACACCAAGGCTGGATGAGTGGGCC-ATCTCAGCTCACTGACCTCACCCTCC 2509
Qy 696 ggggtcaagtattctcctcgcgcagcctcctgagtagctggagactacagcgccacca 755
Dh 2508 GGGGTCAAGTATTTCTCTGCTCAGTCTCCGAGTAGCTGGGATTAACAGCACCCACCA 2449
Qy 756 cgactagtaatt-tttttagtattttagtagatggg-ctccactgcttcagagt 813
Dh 2448 CCATGCCCCGCTCATGTTGATTTTATAGTAGAGAGCGGGTTTCAACATGTTGGCCAGC 2389
Qy 814 tgaacttgatcttgagact--tgtatctgctcctcgcgcctcccaagtgctggagt 871
Dh 2388 TGTCTTGAACTCTCGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 2329
Qy 872 taagagtgtagcacaacagcgccggtc--tattttaatttggtttggttgaatlgaa 929
Dh 2328 TACAGGGGTGAGCAGCCGCGCCACCTAATAAATAATTAATTTATTTTATTTTATTTTATTTT 2269
Qy 930 tctcaactgttaccagctgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 989
Dh 2268 TCTGTCTGTGACACCAAGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2209
Qy 990 cctccgagtgcaagcgaattctcgtctcagcctcccaagcagtgagtgagtgagtgag 1049
Dh 2208 CTTCCCGGGTTTCAACACATCTCTCGTCAAGCTCCGAGTAGCTGGAATTAACAGGCA 2149
Qy 1050 ctgac 1108
Dh 2148 CCAC 2089
Qy 1109 gtcaggtgtgtcctcaactcctcagctcagtgacacacacacacacacacacacacac 1168
Dh 2088 GCCAAGGTAGTCTGATCTCTGACCTCA--TGATCCGCCACACCTCGGCTCCCAAAAGTG 2031

Qy 1169 ctggagattacagggctgtagccacccctccacccagcgggctaattagataaaaaaat 1225
Dh 2030 CTGGATTATACAGCGGTGAGCCACCGCGCCAGCCCATATAAATAATTTTAAAAAAT 1974
RESULT 10
AA163343/c
ID AA163343 standard; DNA: 31853 BP.
XX
AC AA163343;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human kidney related polynucleotide SEQ ID NO 658.
XX
KW Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiast; vasotropic; cerebroprotective;
KW neotropic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; anticancer; vulnery; anticonvulsant; antiparasitic;
KW gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; ds.
XX
OS Homo sapiens.
XX
PN WO200155323-A2.
XX
PD 02-AUG-2001.
XX
PE 17-JAN-2001; 2001WO-US01343.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.

Db	3089	CCGAGTACGCTGGGATTATTAATTTCGGCTCCACACACCTGGCTAACTTT--TGATATTTT	30333
QY	179	agtagagatggaatttctccatgttgcataagctcgtctcgaactccgacatagatga	238
Db	3032	AGTAGAAACGGGGTTTCACCATGTGTGGCCAGGCT-GCTTGAACCTCGACACTGAGTGA	2974
QY	239	ttccctcgtctcggtccctcccaagtgtag----atacgaagctcgcacatgcccgc	294
Db	2973	TCCACTGCTTGGCCCTCCAAAGTGTGGGANTTACAGGGGTGAAGCCACCGCGCCACGT	2914
QY	295	tctgcctcgtctaattttgtcgtagaacaagggttcaactcgaatgctccaaagctgc	354
Db	2913	AATTAATAATATAATTAATTTTGTGAGACGAGAGTCTGCTGTGCGCCAGCGCGGACTG	2854
QY	355	ctgagctcaagcagctcacctcgtccctcagctcccaagtctggtatlaagcgtgaq	414
Db	2853	CGGA----CTCGAGTGGCGGCAATCTGGGCTACATGTGCAAGTCCGGCTTCCGGGTTCACGC	2798
QY	415	ccgtgcctcgtccctttatcttatttttttaagaacacagtgctcccaacttaaccag	474
Db	2797	CATTCTCCTGCTCCTCAGCCTCTAGTAAGCTGGAGCTACAGCGCCGCCACCGCGCCGG	2738
QY	475	atgaagctcagtggtgtgatacag-----ctcacgcagccttca	515
Db	2737	CTAATTTTGTATTTTGTAGTACAGAGGGGTTTCACTTGTATGACGAGATGGTCTCGA	2678
QY	516	actcctcgtagatacagatcctcctcgtcagcctcccaagtgaatctgtagaccaaagatg	575
Db	2677	TCTCCTGACTATG-ATCCACCCGGCTGGCTCCCAAAGTCTGGATTACAGGGGTG	2619
QY	576	caaccatacctcgtgtaattttatattttatattttatgttgaagacagagctctaac	635
Db	2618	AGCCACCGGGCCAGC-----CTTTTTTTTTTTTTTTTTGTGAGACACAGTCTC-AC	2568
QY	636	tctgttaccagaagctcgtgagtgcagtgccgaactctgctcactgcaactcgtcctcc	695
Db	2567	TCTGTACCCAGGCTGGAATGACAGTGGCCC-ATCTAGCTCACTGCACTCTCCACCTCC	2509
QY	696	gggttcaagtattctcctcgtcccaagcctcctcgtagtagctcgtgactacaagcgccaca	755
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QY	756	gcgcctagcctaal-ttttttgtatttttagtagagatgggg-ttcacatgttcgcgaagt	813
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QY	814	tgatcttga tctctggaact--tgtatctcgtcgtcgtccgactcccaagtgctgagt	871
Db	2388	TGCTTGTGAATCTCGACCTCAGGTGATTCACACTGGCTTGCGCTCCCAAAGTCTGGGAT	2329
QY	872	tacagagcgttagaccacacgcgcgcgt--tattttaattttgtttgttgaatgaa	929
Db	2338	TACAGGCGGTGACCCACCGCGCCAGCTATTAATAATTAATTAATTTTGTGACGGAG	2269
QY	930	tctcaactcgttaccagaagctcgtgagatggaatggcaaatctcgtgcctcactgcaactcg	989
Db	2268	TCTCGCTCTGTACCCAGGCTGAGTGCAGTGGTGGCACTGGCTCCTGCTACGCTCAAGGTCA	2209
QY	990	ctctccggagctcaagcgaattctcgttctcaagctcccaagcacaagcctcgtgatatcggcac	1049
Db	2208	CTTCCCGGGTTTCAACACATTTCTGTCCTCAGCGCTCCAGTAGTGGGAATTACAGGCAC	2149
QY	1050	ctgacacacacaccgcgctaa-tttttgtattttcatatagaagcggtttcaccaatatt	1108
Db	2148	CCACACACACACCGGCTAATTTTGTATTTTGTATTAAGACAGCGGGGTTTCACTGTGTTA	2089
QY	1109	gtcagcctcgttctcaaatctcctcgaactcaggtggaaccacactcctcgaactcccaagtg	1168
Db	2088	GCCAGGGTAGTCTGATCTCTGACTCTA--TGATCCGCCACACTGCGCTCCCAAAGTG	2031
QY	1169	ctggagattacagcggtgagccaactcaaccgacggactaatttagataaaaaaat	1225

Db	2030	CTGGGATTACAGCGGTGAGCCACCGCCGACCCCATTAATAATTTTAAAAAT	1974
RESULT	11		
ID	AAS39682/c		
XX	AAS39682 standard; DNA; 11319 BP.		
XX	AAS39682;		
XX			
DT	17-DEC-2001 (first entry)		
XX			
DE	Genomic sequence #101 encoding human colon associated polypeptide.		
XX			
KW	Human; colon cancer; congenital abnormality; infection; colitis;		
KW	Inflammatory bowel disease; IBD; neoplastic disorder; gene therapy;		
KW	intestinal inflammatory disorder; malabsorption syndrome; gastric;		
KW	sigmoid disease; antibacterial; antiviral; antiinflammatory;		
XX	cytostatic; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200155302-A2.		
XX			
PD	02-AUG-2001.		
XX			
PF	17-JAN-2001; 2001WO-US01240.		
XX			
PR	31-JAN-2000; 2000US-0179065.		
PR	04-FEB-2000; 2000US-0180628.		
PR	24-FEB-2000; 2000US-0184664.		
PR	02-MAR-2000; 2000US-0186350.		
PR	16-MAR-2000; 2000US-0189874.		
PR	17-MAR-2000; 2000US-0190076.		
PR	18-APR-2000; 2000US-0198123.		
PR	19-MAY-2000; 2000US-0205315.		
PR	07-JUN-2000; 2000US-0209467.		
PR	28-JUN-2000; 2000US-0214886.		
PR	30-JUN-2000; 2000US-0215135.		
PR	07-JUL-2000; 2000US-0216647.		
PR	07-JUL-2000; 2000US-0216880.		
PR	11-JUL-2000; 2000US-0217487.		
PR	11-JUL-2000; 2000US-0217496.		
PR	14-JUL-2000; 2000US-0218290.		
PR	26-JUL-2000; 2000US-0220963.		
PR	26-JUL-2000; 2000US-0220964.		
PR	14-AUG-2000; 2000US-0224518.		
PR	14-AUG-2000; 2000US-0224519.		
PR	14-AUG-2000; 2000US-0225213.		
PR	14-AUG-2000; 2000US-0225214.		
PR	14-AUG-2000; 2000US-0225266.		
PR	14-AUG-2000; 2000US-0225267.		
PR	14-AUG-2000; 2000US-0225268.		
PR	14-AUG-2000; 2000US-0225447.		
PR	14-AUG-2000; 2000US-0225447.		
PR	14-AUG-2000; 2000US-0225757.		
PR	14-AUG-2000; 2000US-0225758.		
PR	14-AUG-2000; 2000US-0225759.		
PR	18-AUG-2000; 2000US-0226279.		
PR	22-AUG-2000; 2000US-0226681.		
PR	22-AUG-2000; 2000US-0226868.		
PR	22-AUG-2000; 2000US-0227182.		
PR	23-AUG-2000; 2000US-0227009.		
PR	30-AUG-2000; 2000US-0228924.		
PR	01-SEP-2000; 2000US-0229287.		
PR	01-SEP-2000; 2000US-0229343.		
PR	01-SEP-2000; 2000US-0229344.		
PR	01-SEP-2000; 2000US-0229345.		
PR	05-SEP-2000; 2000US-0229509.		
PR	05-SEP-2000; 2000US-0229513.		
PR	06-SEP-2000; 2000US-0230437.		
PR	06-SEP-2000; 2000US-0230438.		
PR	08-SEP-2000; 2000US-0231242.		
PR	08-SEP-2000; 2000US-0231243.		
PR			

[illegible]

CC cytokinesis or the cell cycle, or inhibit the proliferation in a cancer
 CC cell by inhibiting the cell with the antisense oligonucleotide.
 CC A581531-A581768 represent Survivin nucleic acids, and antisense
 CC oligonucleotides targeted to Survivin, used in the method of the
 CC invention.
 CC
 SO Sequence 14796 BP; 3482 A; 3488 C; 3888 G; 3938 T; 0 other;

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